Amendments to the Claims:

Please cancel claims 1, 2, 6, 7, 19, 53-57 and 75-91 without prejudice or disclaimer, and please enter new claims 92-164 as set forth in the complete listing of the claims that follows. This complete listing of the claims replaces previous claim listings.

1-91 (cancelled).

92 (new). A method for determining whether a human subject is at an increased risk or decreased risk of breast cancer, which comprises:

(a) detecting in a nucleic acid of the human subject the presence of a polymorphic variant selected from the group consisting of a guanine corresponding to position 7573 of SEQ ID NO: 2, a guanine corresponding to position 13903 of SEQ ID NO: 2, an adenine corresponding to position 23826 of SEQ ID NO: 2, an adenine corresponding to position 26057 of SEQ ID NO: 2, a thymine corresponding to position 26361 of SEQ ID NO: 2, an adenine corresponding to position 26599 of SEQ ID NO: 2, an adenine corresponding to position 26812 of SEQ ID NO: 2, a cytosine corresponding to position 27069 of SEQ ID NO: 2, an adenine corresponding to position 35127 of SEQ ID NO: 2, a thymine corresponding to position 35222 of SEQ ID NO: 2, a cytosine corresponding to position 36424 of SEQ ID NO: 2, a cytosine corresponding to position 46176 of SEQ ID NO: 2, a cytosine corresponding to position 50452 of SEQ ID NO: 2, a guanine corresponding to position 61093 of SEQ ID NO: 2, an adenine corresponding to position 62572 of SEQ ID NO: 2, a guanine corresponding to position 70759 of SEQ ID NO: 2, and a complement of the foregoing; or

(b) detecting in a nucleic acid of the human subject the presence of a polymorphic variant selected from the group consisting of an adenine corresponding to position 7573 of SEQ ID NO: 2, a cytosine corresponding to position 13903 of SEQ ID NO: 2, a thymine corresponding to position 23826 of SEQ ID NO: 2, a guanine corresponding to position 26057 of SEQ ID NO: 2, a

cytosine corresponding to position 26361 of SEQ ID NO: 2, a guanine corresponding to position 26599 of SEQ ID NO: 2, a guanine corresponding to position 26812 of SEQ ID NO: 2, a thymine corresponding to position 27069 of SEQ ID NO: 2, a guanine corresponding to position 35127 of SEQ ID NO: 2, a guanine corresponding to position 35222 of SEQ ID NO: 2, a thymine corresponding to position 36424 of SEQ ID NO: 2, a guanine corresponding to position 46176 of SEQ ID NO: 2, a thymine corresponding to position 50452 of SEQ ID NO: 2, a cytosine corresponding to position 61093 of SEQ ID NO: 2, a guanine corresponding to position 62572 of SEQ ID NO: 2, an adenine corresponding to position 70759 of SEQ ID NO: 2, and a complement of the foregoing;

whereby it is determined that the subject is at an increased risk of breast cancer based on the presence of one or more of the polymorphic variants of (a), and whereby it is determined that the subject is at a decreased risk of breast cancer based on the presence of one or more of the polymorphic variations of (b).

93 (new). The method of claim 92, which further comprises obtaining the nucleic acid sample from the subject.

94 (new). The method of claim 92, wherein detecting the presence of the one or more polymorphic variants comprises:

hybridizing an oligonucleotide to the nucleic acid from the subject, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variant;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence a polymorphic variant in the extension products.

95 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 7573 of SEQ ID NO: 2, or a complement thereof.

96 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 13903 of SEQ ID NO: 2, or a complement thereof.

97 (new). The method of claim 92, wherein the polymorphic variant detected is an adenine corresponding to position 23826 of SEQ ID NO: 2, or a complement thereof.

98 (new). The method of claim 92, wherein the polymorphic variant detected is an adenine corresponding to position 26057 of SEQ ID NO: 2, or a complement thereof.

99 (new). The method of claim 92, wherein the polymorphic variant detected is a thymine corresponding to position 26361 of SEQ ID NO: 2, or a complement thereof.

100 (new). The method of claim 92, wherein the polymorphic variant detected is an adenine corresponding to position 26599 of SEQ ID NO: 2, or a complement thereof.

101 (new). The method of claim 92, wherein the polymorphic variant detected is an adenine corresponding to position 26812 of SEQ ID NO: 2, or a complement thereof.

102 (new). The method of claim 92, wherein the polymorphic variant detected is a cytosine corresponding to position 27069 of SEQ ID NO: 2, or a complement thereof.

103 (new). The method of claim 92, wherein the polymorphic variant detected is an adenine corresponding to position 35127 of SEQ ID NO: 2, or a complement thereof.

104 (new). The method of claim 92, wherein the polymorphic variant detected is a thymine corresponding to position 35222 of SEQ ID NO: 2, or a complement thereof.

105 (new). The method of claim 92, wherein the polymorphic variant detected is a cytosine corresponding to position 36424 of SEQ ID NO: 2, or a complement thereof.

106 (new). The method of claim 92, wherein the polymorphic variant detected is a cytosine corresponding to position 46176 of SEQ ID NO: 2, or a complement thereof.

107 (new). The method of claim 92, wherein the polymorphic variant detected is a cytosine corresponding to position 50452 of SEQ ID NO: 2, or a complement thereof.

108 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 61093 of SEQ ID NO: 2, or a complement thereof.

109 (new). The method of claim 92, wherein the polymorphic variant detected is an adenine corresponding to position 62572 of SEQ ID NO: 2, or a complement thereof.

110 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 70759 of SEQ ID NO: 2, or a complement thereof.

111 (new). The method of claim 92, wherein the polymorphic variant detected is an adenine corresponding to position 7573 of SEQ ID NO: 2, or a complement thereof.

112 (new). The method of claim 92, wherein the polymorphic variant detected is a cytosine corresponding to position 13903 of SEQ ID NO: 2, or a complement thereof.

113 (new). The method of claim 92, wherein the polymorphic variant detected is a thymine corresponding to position 23826 of SEQ ID NO: 2, or a complement thereof.

114 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 26057 of SEQ ID NO: 2, or a complement thereof.

115 (new). The method of claim 92, wherein the polymorphic variant detected is a cytosine corresponding to position 26361 of SEQ ID NO: 2, or a complement thereof.

116 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 26599 of SEQ ID NO: 2, or a complement thereof.

117 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 26812 of SEQ ID NO: 2, or a complement thereof.

118 (new). The method of claim 92, wherein the polymorphic variant detected is a thymine corresponding to position 27069 of SEQ ID NO: 2, or a complement thereof.

119 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 35127 of SEQ ID NO: 2, or a complement thereof.

120 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 35222 of SEQ ID NO: 2, or a complement thereof.

121 (new). The method of claim 92, wherein the polymorphic variant detected is a thymine corresponding to position 36424 of SEQ ID NO: 2, or a complement thereof.

122 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 46176 of SEQ ID NO: 2, or a complement thereof.

123 (new). The method of claim 92, wherein the polymorphic variant detected is a thymine corresponding to position 50452 of SEQ ID NO: 2, or a complement thereof.

124 (new). The method of claim 92, wherein the polymorphic variant detected is a cytosine corresponding to position 61093 of SEQ ID NO: 2, or a complement thereof.

125 (new). The method of claim 92, wherein the polymorphic variant detected is a guanine corresponding to position 62572 of SEQ ID NO: 2, or a complement thereof.

126 (new). The method of claim 92, wherein the polymorphic variant detected is an adenine corresponding to position 70759 of SEQ ID NO: 2, or a complement thereof.

127 (new). The method of claim 92, wherein the human subject is Caucasian.

128 (new). A method for determining whether a breast cancer detection procedure is administered to a human subject, which comprises:

(a) detecting in a nucleic acid of the human subject the presence of a polymorphic variant selected from the group consisting of a guanine corresponding to position 7573 of SEQ ID NO: 2, a guanine corresponding to position 13903 of SEQ ID NO: 2, an adenine corresponding to position 23826 of SEQ ID NO: 2, an adenine corresponding to position 26057 of SEQ ID NO: 2, a thymine corresponding to position 26361 of SEQ ID NO: 2, an adenine corresponding to position 26599 of SEQ ID NO: 2, an adenine corresponding to position 26812 of SEQ ID NO: 2, a cytosine corresponding to position 27069 of SEQ ID NO: 2, an adenine corresponding to position 35127 of SEQ ID NO: 2, a thymine corresponding to position 35222 of SEQ ID NO: 2, a cytosine corresponding to position 36424 of SEQ ID NO: 2, a cytosine corresponding to position 46176 of SEQ ID NO: 2, a cytosine corresponding to position 50452 of SEQ ID NO: 2, a guanine corresponding to position 61093 of SEQ ID NO: 2, an adenine corresponding to position 62572 of SEQ ID NO: 2, a guanine corresponding to position 70759 of SEQ ID NO: 2, and a complement of the foregoing; or

(b) detecting in a nucleic acid of the human subject the presence of a polymorphic variant selected from the group consisting of an adenine corresponding to position 7573 of SEQ ID NO: 2, a cytosine corresponding to position 13903 of SEQ ID NO: 2, a thymine corresponding to position 23826 of SEQ ID NO: 2, a guanine corresponding to position 26057 of SEQ ID NO: 2, a cytosine corresponding to position 26361 of SEQ ID NO: 2, a guanine corresponding to position 26599 of SEQ ID NO: 2, a guanine corresponding to position 26812 of SEQ ID NO: 2, a thymine corresponding to position 27069 of SEQ ID NO: 2, a guanine corresponding to position 35127 of SEQ ID NO: 2, a guanine corresponding to position 35222 of SEQ ID NO: 2, a thymine

corresponding to position 36424 of SEQ ID NO: 2, a guanine corresponding to position 46176 of SEQ ID NO: 2, a thymine corresponding to position 50452 of SEQ ID NO: 2, a cytosine corresponding to position 61093 of SEQ ID NO: 2, a guanine corresponding to position 62572 of SEQ ID NO: 2, an adenine corresponding to position 70759 of SEQ ID NO: 2, and a complement of the foregoing; and

administering a breast cancer detection procedure to a human subject determined to have an increased risk of breast cancer based on the presence of the one or more polymorphic variants of (a), or not administering a breast cancer detection procedure to a human subject determined to have a decreased risk of breast cancer based on the presence of the one or more polymorphic variants of (b).

129 (new). The method of claim 128, which further comprises obtaining the nucleic acid sample from the subject.

130 (new). The method of claim 128, wherein detecting the presence of the one or more polymorphic variants comprises:

hybridizing an oligonucleotide to the nucleic acid from the subject, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variant;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence a polymorphic variant in the extension products.

131 (new). The method of claim 128, wherein the breast cancer detection procedure is selected from the group consisting of a mammography, an early mammography program, a frequent mammography program, a biopsy procedure, a breast biopsy and biopsy from another tissue, a breast ultrasound and optionally ultrasound analysis of another tissue, breast magnetic resonance

imaging (MRI) and optionally MRI analysis of another tissue, electrical impedance (T-scan) analysis of breast and optionally of another tissue, ductal lavage, nuclear medicine analysis, scintimammography, *BRCA1* and/or *BRCA2* sequence analysis results, thermal imaging of the breast and optionally of another tissue, and a combination of the foregoing.

132 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 7573 of SEQ ID NO: 2, or a complement thereof.

133 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 13903 of SEQ ID NO: 2, or a complement thereof.

134 (new). The method of claim 128, wherein the polymorphic variant detected is an adenine corresponding to position 23826 of SEQ ID NO: 2, or a complement thereof.

135 (new). The method of claim 128, wherein the polymorphic variant detected is an adenine corresponding to position 26057 of SEQ ID NO: 2, or a complement thereof.

136 (new). The method of claim 128, wherein the polymorphic variant detected is a thymine corresponding to position 26361 of SEQ ID NO: 2, or a complement thereof.

137 (new). The method of claim 128, wherein the polymorphic variant detected is an adenine corresponding to position 26599 of SEQ ID NO: 2, or a complement thereof.

138 (new). The method of claim 128, wherein the polymorphic variant detected is an adenine corresponding to position 26812 of SEQ ID NO: 2, or a complement thereof.

139 (new). The method of claim 128, wherein the polymorphic variant detected is a cytosine corresponding to position 27069 of SEQ ID NO: 2, or a complement thereof.

140 (new). The method of claim 128, wherein the polymorphic variant detected is an adenine corresponding to position 35127 of SEQ ID NO: 2, or a complement thereof.

141 (new). The method of claim 128, wherein the polymorphic variant detected is a thymine corresponding to position 35222 of SEQ ID NO: 2, or a complement thereof.

142 (new). The method of claim 128, wherein the polymorphic variant detected is a cytosine corresponding to position 36424 of SEQ ID NO: 2, or a complement thereof.

143 (new). The method of claim 128, wherein the polymorphic variant detected is a cytosine corresponding to position 46176 of SEQ ID NO: 2, or a complement thereof.

144 (new). The method of claim 128, wherein the polymorphic variant detected is a cytosine corresponding to position 50452 of SEQ ID NO: 2, or a complement thereof.

145 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 61093 of SEQ ID NO: 2, or a complement thereof.

146 (new). The method of claim 128, wherein the polymorphic variant detected is an adenine corresponding to position 62572 of SEQ ID NO: 2, or a complement thereof.

147 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 70759 of SEQ ID NO: 2, or a complement thereof.

148 (new). The method of claim 128, wherein the polymorphic variant detected is an adenine corresponding to position 7573 of SEQ ID NO: 2, or a complement thereof.

149 (new). The method of claim 128, wherein the polymorphic variant detected is a cytosine corresponding to position 13903 of SEQ ID NO: 2, or a complement thereof.

150 (new). The method of claim 128, wherein the polymorphic variant detected is a thymine corresponding to position 23826 of SEQ ID NO: 2, or a complement thereof.

151 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 26057 of SEQ ID NO: 2, or a complement thereof.

152 (new). The method of claim 128, wherein the polymorphic variant detected is a cytosine corresponding to position 26361 of SEQ ID NO: 2, or a complement thereof.

153 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 26599 of SEQ ID NO: 2, or a complement thereof.

154 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 26812 of SEQ ID NO: 2, or a complement thereof.

155 (new). The method of claim 128, wherein the polymorphic variant detected is a thymine corresponding to position 27069 of SEQ ID NO: 2, or a complement thereof.

156 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 35127 of SEQ ID NO: 2, or a complement thereof.

157 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 35222 of SEQ ID NO: 2, or a complement thereof.

158 (new). The method of claim 128, wherein the polymorphic variant detected is a thymine corresponding to position 36424 of SEQ ID NO: 2, or a complement thereof.

159 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 46176 of SEQ ID NO: 2, or a complement thereof.

160 (new). The method of claim 128, wherein the polymorphic variant detected is a thymine corresponding to position 50452 of SEQ ID NO: 2, or a complement thereof.

161 (new). The method of claim 128, wherein the polymorphic variant detected is a cytosine corresponding to position 61093 of SEQ ID NO: 2, or a complement thereof.

162 (new). The method of claim 128, wherein the polymorphic variant detected is a guanine corresponding to position 62572 of SEQ ID NO: 2, or a complement thereof.

163 (new). The method of claim 128, wherein the polymorphic variant detected is an adenine corresponding to position 70759 of SEQ ID NO: 2, or a complement thereof.

164 (new). The method of claim 128, wherein the human subject is Caucasian.